

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Sandman, Olga  
Hawkins, Phillip R.  
Hillman, Jennifer L.  
Lal, Preeti  
Goli, Surya K.
- (ii) TITLE OF THE INVENTION: NOVEL HUMAN SERINE  
CARBOXYPEPTIDASE
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Filed Herewith
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0241 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) IMMEDIATE SOURCE:
  - (A) LIBRARY: MPMONOT13
  - (B) CLONE: 442014

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
1				5					10					15	
Pro	Gly	Pro	Cys	Asp	Gly	Leu	Phe	His	Ser	Leu	Tyr	Arg	Ser	Val	Ser
			20					25					30		
Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
			35				40					45			
Ile	Glu	Ala	Gly	Lys	Ile	Gln	Lys	Gly	Arg	Glu	Leu	Ser	Leu	Val	Gly
	50					55					60				
Pro	Phe	Pro	Gly	Leu	Asn	Met	Lys	Ser	Tyr	Ala	Asp	Phe	Leu	Thr	Val
65					70					75					80
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85				90						95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Glu	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
			115				120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165				170						175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215						220			
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225					230					235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245				250						255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
		275				280						285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
			325					330					335		
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		
Thr	Ile	Val	Glu	Lys	Tyr	Leu	Arg	Glu	Asp	Thr	Val	Gln	Ser	Val	Lys
	355					360						365			
Pro	Trp	Leu	Thr	Glu	Ile	Met	Asn	Asn	Tyr	Lys	Val	Leu	Ile	Tyr	Asn
	370					375					380				
Gly	Gln	Leu	Asp	Ile	Ile	Val	Ala	Ala	Ala	Leu	Thr	Glu	Arg	Ser	Leu
385					390					395					400
Met	Gly	Met	Asp	Trp	Lys	Gly	Ser	Gln	Gln	Tyr	Lys	Lys	Ala	Glu	Lys
			405					410					415		
Lys	Lys	Val	Trp	Lys	Ile	Phe	Lys	Ser	Asp	Ser	Gly	Val	Ala	Gly	Tyr
			420					425					430		
Ile	Arg	Gln	Val	Gly	Asp	Phe	His	Gln	Val	Ile	Ile	Arg	Gly	Gly	Gly
	435					440						445			
His	Thr	Leu	Pro	Tyr	Asp	Gln	Pro	Leu	Arg	Ala	Phe	Asp	Met	Ile	Asn

450                      455                      460  
 Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465                      470                      475

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MPHENOT03  
 (B) CLONE: 443004

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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AAGCGCTGCA AGGACAACCG GCTGGGGTCC TTGGGGGGGG GGCTCAGGGA CCAGCACCGA      60
CTGCGCCGCA CCTGAGAGA TGGTTGGTGC CATGTGGAAG GTGATTGTTT CGCTGGTCTT      120
GTTGATGCCT GGGCCCTGTG ATGGGCTGTT TCACTCCCTA TACAGAAGTG TTTCCATGCC      180
ACCTAAGGGA GACTCAGGAC AGCCATTATT TCTCACCCCT TACATTGAAG CTGGGAAGAT      240
CCAAAAAGGA AGAGAATTGA GTTGGGTGGG TCCTTTTCCA GGAAGTGAACA TGAAGAGTTA      300
TGCCGACTTC CTCACTGTGA ATAAGACTTA CAACAGCAAC CTCTTCTTCT GGTTCCTTCC      360
AGCTCAGATA CAGCCAGAAG ATGCCCCAGT AGTTCTCTGG CTACAGGGTG AGCCGGGAGG      420
TTCATCCATG TTTGGACTCT TTGTGGAACA TGGGCTTTAT GTTGTCACAA GTAACATGAC      480
CTTGCGTGAC AGAGACTTCC CCTGGACCAC AACGCTCTCC ATGCTTTACA TTGACAATCC      540
AGTGGGCACA GGCTTCAGTT TTAAGTATGA TACCCACGGA TATGCAGTCA ATGAGGACGA      600
TGTAAGCAAG GATTTATACA GTGCACTAAT TCAGTTTTTC CAGATATTTT CTGAATATAA      660
AAATAATGAC TTTTATGTCA CTGGGGAGTC TTATGCAGGG AAATATGTGC CAGCCATTGC      720
ACACCTCATC CATTCCTCCA ACCCTGTGAG AGAGGTGAAG ATCAACCTGA ACGGAATTGC      780
TATTGGAGAT GGATATTTCTG ATCCCGAATC AATTATAGGG GGCTATGCAG AATTCCTGTA      840
CCAAATTTGGC TTGTTTGGATG AGAAGCAAAA AAAGTACTTC CAGAAGCAGT GCCATGAATG      900
CATAGAACAC ATCAGGAAGC AGAACTGGTT TGAGGCTTTT GAAATACTGG ATAACTACT      960
AGATGGCGAC TTAACAAGTG ATCCTTCTTA CTTCAGAAAT GTTACAGGAT GTAGTAATTA     1020
CTATAACTTT TTGCGGTGCA CGAACCCTGA GGATCAGCTT TACTATGTGA AATTTTTGTC     1080
ACTCCACAGG GTGAGACAAG CCATCCACGT GGGGAATCAG ACTTTTAATG ATGGAACAT      1140
AGTTGAAAAG TACTTGGGAG AAGATACAGT ACAGTCAGTT AAGCCATGGT TAACGTAAAT      1200
CATGAATAAT TATAAGGTTT TGATCTACAA TGGCCAACTG GACATCATCG TGGCAGCTGC     1260
CCTGACAGAG CGCTCCTTGA TGGGCATGGA CTGGAAAAGG TCCCAGGAAT ACAAGAAGGC     1320
AGAAAAAAAA AAAGTTTGGG AGATCTTTAA ATCTGACAGT GGAGTGGCTG GTTACATCCG     1380
GCAAGTGGGT GACTTCCATC AGTAAATTAT TCGAGGTGGA GGACATACTT TACCCTATGA     1440
CCAGCCTCTG AGAGCTTTTG ACATGATTAA TCGATTCAAT TATGGAAAAG GATGGGATCC     1500
TTATGTTGGA TAACTACCT TCCAAAAGA GAACATCAGA GGTTTTTCAT GCTGAAAAGA     1560
AAATCGTAAA AACAGAAAAT GTCATAGGAA TAAAAAATT ATCTTTTCAT ATCTGCAAGA     1620
TCTTTTTCAT CAATAAAAAT TATCCTTGAA ACAAAAAAAA AAAGAAAAAG      1670

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MMLR3DT11  
 (B) CLONE: 566993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
1				5					10					15	
Pro	Gly	Pro	Cys	Asp	Gly	Leu	Phe	His	Ser	Leu	Tyr	Arg	Ser	Val	Ser
			20					25					30		
Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
			35				40					45			
Ile	Glu	Ala	Gly	Lys	Ile	Gln	Lys	Gly	Arg	Glu	Leu	Ser	Leu	Val	Gly
	50					55					60				
Pro	Phe	Pro	Gly	Leu	Asn	Met	Lys	Ser	Tyr	Ala	Gly	Phe	Leu	Thr	Val
65					70					75					80
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85				90					95		
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Xaa	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
			115				120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Xaa	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165				170						175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225				230						235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245				250						255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260				265						270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
	275					280						285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325				330					335		
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		
Thr	Ile	Val	Glu	Lys	Tyr	Leu	Arg	Glu	Asp	Thr	Val	Gln	Ser	Val	Lys
	355					360						365			
Pro	Trp	Leu	Thr	Glu	Ile	Met	Asn	Asn	Tyr	Lys	Val	Leu	Ile	Tyr	Asn
	370					375					380				
Gly	Gln	Leu	Asp	Ile	Ile	Val	Ala	Ala	Ala	Leu	Thr	Glu	Arg	Ser	Leu
385				390						395					400
Met	Gly	Met	Asp	Trp	Lys	Gly	Ser	Gln	Glu	Tyr	Lys	Lys	Ala	Glu	Lys
				405				410					415		
Lys	Val	Trp	Lys	Ile	Phe	Lys	Ser	Asp	Ser	Glu	Val	Ala	Gly	Tyr	Ile
	420						425						430		
Arg	Gln	Val	Gly	Asp	Phe	His	Gln	Val	Ile	Ile	Arg	Gly	Gly	Gly	His
	435					440						445			
Ile	Leu	Pro	Tyr	Asp	Gln	Pro	Leu	Arg	Ala	Phe	Asp	Met	Ile	Asn	Arg

450                                      455                                      460  
 Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465                                      470                                      475

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MMLR3DT01
- (B) CLONE: 564993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

GAAAGCTGGT ACGCCTGCNG GTNCCGGTCC GGAATTGNGG GGTNGACCCA CCGCTCCGAN      60
CGACTGCGCC GCACCCCTGAG AGATGGTTGG TGCCATGTGG AAGGTGATTG TTTCGCTGGT      120
CCTGTTGATG CCTGCGCCCT GTGATGGGCT GTTTCCTCC CTATACAGAA GTGTTTCCAT      180
GCCACCTAAG GGAGACTCAG GACAGCCATT ATTTCTCACC CCTTACATTG AAGCTGGGAA      240
GATCCAAAAA GGAAGAGAAAT TGAGTTTGGT CGGCCCTTTC CCAGGACTGA ACATGAAGAG      300
TTATGCGCGC TTCTTCACCG TGAATAAGAC TTACAACAGC AACCTCTTCT TCTGGTTCTT      360
CCCAGCTCAG ATACAGCCAG AAGATGCCCC AGTAGTTCTC TGGCTACAGG GTGGGCCCGG      420
AGGTTTCATC ATGTTWGGAC TCTTTGTGGA ACATGGGCTT TATGTTGTCA CAAGTAACAT      480
GACCTTGCGT GACAGAGACT TCCCCTGGAC CACAACGCTC TCCATGCTTT ACATTGACAA      540
TCCAGTGGGC ACAGGCTTCA GTTTTACTGA TGATACCCAC GGATATGCAG TCAATGAGGA      600
CGATGTAGCA CGGGATTTAT ACAGTGCCTT AATTCAGTTT TTCCAGATAT TTCTGAATA      660
TAAAAATAAT GACTTTTATG TCACTGGGGA GTCTTATGCA GGGAAATATG TGCCAGCCAT      720
TGCACACCTC ATCCATTCCC TCAACCTGTG GAGAGAGGTG AAGATCAACC TGAACCGAAT      780
TGCTATTGGA GATGGATATT CTGATCCCGA ATCAATTATA GGGGGCTATG CAGAATTCCCT      840
GTACCAAAAT GGCTGTGTTG ATGAGAAGCA AAAAAAGTAC TTCCAGAAGC AGTGCCATGA      900
ATGCATAGAA CACATCAGGA AGCAGAACTG GTTTGAGGCC TTGAAATAC TGGATAAACT      960
ACTAGATGGC GACTTAACAA GTGATCCTTC TTACTTCCAG AATGTTACAG GATGTAGTAA     1020
TTACTATAAC TTTTTCGGGT GCACGGAACC TGAGSATCAG CTTTACTATG TGAAATTTTT     1080
GTCACTCCCA GAGTGGAGAC AAGCCATCCA CGTGGGGAAT CAGACTTTTA ATGATGGAAC     1140
TATAGTTGAA AAGTACTTGC GAGAAGATAC AGTACAGTCA GTTAAGCCAT GGTTAACCTGA     1200
AATCATGAAT AATTATAAGG TTCTGATCTA CAATGGCCAA CTGGACATCA TCGTGGCAGC     1260
TGCCCTGACA GAGGCTCTCT TGATGGGCTT GGACTGGAAA GGTTCCTCAGG AATACAAGAA     1320
GGCAGAAAAA AAAGTTTGGA AGATCTTTAA ATCTGACAGT GAAGTGGCTG GTTACATCCG     1380
GCAAGTGGGT GACTTCCATC AGGTAAATTAT TCGAGGTGGA GGACATATTT TACCCATATGA     1440
CCAGCCTCTG AGAGCTTTTG ACATGATTAA TCGATTCAAT TATGGAAAAG GATGGGATCC     1500
TTATGTTGGA TAACTACCT TCCAAAAAGA GAACATCAGA GGTTTTCATN T      1561

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## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNCRF01
- (B) CLONE: TUP469

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
1				5				10					15		
Pro	Gly	Pro	Cys	Gly	Gly	Leu	Phe	His	Ser	Leu	Tyr	Arg	Ser	Val	Ser
			20					25					30		
Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
			35				40					45			
Ile	Glu	Ala	Gly	Lys	Ile	Tyr	Thr	Gly	Thr	Asn	Ser	Val	Phe	Gln	Ile
	50				55					60					
Phe	Pro	Glu	Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr
65				70					75					80	
Ala	Gly	Lys	Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn
				85				90						95	
Pro	Val	Arg	Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp
			100					105					110		
Gly	Tyr	Ser	Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu
	115						120					125			
Tyr	Gln	Ile	Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys
	130					135					140				
Gln	Cys	His	Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu
145				150					155					160	
Ala	Phe	Glu	Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp
				165					170					175	
Pro	Ser	Tyr	Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe
			180					185						190	
Leu	Arg	Cys	Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu
	195					200						205			
Ser	Leu	Pro	Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe
	210					215					220				
Asn	Asp	Gly	Thr	Ile	Val	Glu	Lys	Tyr	Leu	Arg	Glu	Asp	Thr	Val	Gln
225				230					235					240	
Ser	Val	Lys	Pro	Trp	Leu	Thr	Glu	Ile	Met	Asn	Asn	Tyr	Lys	Val	Leu
			245					250						255	
Ile	Tyr	Asn	Gly	Gln	Leu	Asp	Ile	Ile	Val	Ala	Ala	Ala	Leu	Thr	Glu
	260						265						270		
Arg	Ser	Leu	Met	Gly	Met	Asp	Trp	Lys	Gly	Ser	Gln	Glu	Tyr	Lys	Lys
	275					280						285			
Ala	Glu	Lys	Lys	Val	Trp	Lys	Ile	Phe	Lys	Ser	Asp	Ser	Glu	Val	Ala
	290					295					300				
Gly	Tyr	Ile	Arg	Gln	Val	Gly	Asp	Phe	His	Gln	Val	Ile	Ile	Arg	Gly
305				310					315					320	
Gly	Gly	His	Ile	Leu	Pro	Tyr	Asp	Gln	Pro	Leu	Arg	Ala	Phe	Asp	Met
			325					330						335	
Ile	Asn	Arg	Phe	Ile	Tyr	Gly	Lys	Gly	Trp	Asp	Pro	Tyr	Val	Gly	
			340					345					350		

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNCRT01
- (B) CLONE: 770469

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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AAGGCAAACC GGCTGGGGTC CTTGGGGGCG GGGGCTCAGG GAGGAGCACC GAETGCCCCG      50
CACCCGTGAGA GATGGTTGGT GCCAGTGGGA AGGTGATTGT TTGGCTGGTC CTGTTGATGC      100
CTGGCCCCCG TGCTGGGGTC TTTCACCTCC TATACAGAAG TGTTTCCATG CCACCPAAGG      150
GAGACTCAGG ACAGCCATTA TTTCACCCC CTTACATTGA AGCTGGGAAG ATTTATACAG      200
GCACTAATTC AGTTTCCAG ATATTCCCTG AATATAAAAA TAATGACTTT TATGTCACTG      250
GGGAGTCCTTA TCCAGGGAAA TADGTGCCAG CCATTGACCA CCTCATCCAT TCCCTCAACC      300
CTGTGAGAGA GGTGAAGATC AACCTGAACG GAATTGCTAT TGGAGATGGA TATCTGATC      350
CCGAATCAAT TATAGGGGGC TATGACAGAT TCCGTACCCA AATTGGCTTG TTGGATGAGA      400
AGCAAAAAAA GTACTTCCAG AAGCAGTGCC ATGAATGCAT AGAACACATC AGGAAGCAGA      450
ACTGGTTTGA GGCCTTTGAA ATACTGGATA AACTACTAGA TGGCGACTTA ACAAGTGATC      500
CTTCTTACTT CCAGAAATGT ACAGGATGTA GTAATTACTA TAACTTTTTG CGGTGCACGG      550
AACCTGAGGA TCAGCTTTAC TATGTGAAAT TTTTGTCACT CCCAGAGGTG AGACAAGCCA      600
TCCACGTGGG GAATCAGACT TTTAATGATG GAATATAGT TGAAAAGTAC TPGCGAGAAG      650
ATACAGTACA GTCAGTTAAG CCATGTTTAA CTGAAATCAT GAATAATTAT AAGGTTCTGA      700
TCTACAATGG CCAACTGGAC ATCATCGTGG CAGCTGCCCT GACAGAGCGC TCCTTGATGG      750
GCATGGACTG GAAAGGATCC CAGGAATACA AGAAGGCAGA AAAAAAAGTT TGGGAAGATCT      800
TTAAATCTGA CAGTGAAGTG GCTGGTTACA TCCCGCAAGT GGGTGAAGTC CATCAGGTAA      850
TTATTCGAGG TGGAGGACAT ATTTTACCC TATGACAGCC TCTGAGAGCT TTTGACATGA      900
TTAATCGATT CATTTATGGA AAAGGATGGG ATCCTTATGT TGGATAAAGT ACCTTCCCAA      950
AAGAGAACAT CAGAGGTTTT CATTGCTGAA AAGAAAATCG TAAAAACAGA AAATGTCATA      1000
GGAATAAAAA AATTATCTTT TCATATCTGC AAGATTTTTT TCATCAATAA AAATTATCCT      1050
TGA                                                                                   1063

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## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1713107

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Val Lys Phe His Leu Leu Val Leu Ile Ala Phe Thr Cys Tyr Thr
 1             5             10             15
Cys Ser Asp Ala Thr Leu Trp Asn Pro Tyr Lys Lys Leu Met Arg Gly
 20             25             30
Ser Ala Ser Pro Pro Arg Pro Gly Glu Ser Gly Glu Pro Leu Phe Leu
 35             40             45
Thr Pro Leu Leu Gln Asp Gly Lys Ile Glu Glu Ala Arg Asn Lys Ala
 50             55             60
Arg Val Asn His Pro Met Leu Ser Ser Val Glu Ser Tyr Ser Gly Phe
 65             70             75             80
Met Thr Val Asp Ala Lys His Asn Ser Asn Leu Phe Phe Trp Tyr Val
 85             90             95
Pro Ala Lys Asn Asn Arg Glu Gln Ala Pro Ile Leu Val Trp Leu Gln
100             105             110
Gly Gly Pro Gly Ala Ser Ser Leu Phe Gly Met Phe Glu Glu Asn Gly
115             120             125
Pro Phe His Ile His Arg Asn Lys Ser Val Lys Gln Arg Glu Tyr Ser
130             135             140
Trp His Gln Asn His His Met Ile Tyr Ile Asp Asn Pro Val Gly Thr
145             150             155             160
Gly Phe Ser Phe Thr Asp Ser Asp Glu Gly Tyr Ser Thr Asn Glu Glu
165             170             175

```

His Val Gly Glu Asn Leu Met Lys Phe Ile Gln Gln Phe Phe Val Leu  
 180 185 190  
 Phe Pro Asn Leu Leu Lys His Pro Phe Tyr Ile Ser Gly Glu Ser Tyr  
 195 200 205  
 Gly Gly Lys Phe Val Pro Ala Phe Gly Tyr Ala Ile His Asn Ser Gln  
 210 215 220  
 Ser Gln Pro Lys Ile Asn Leu Gln Gly Leu Ala Ile Gly Asp Gly Tyr  
 225 230 235 240  
 Thr Asp Pro Leu Asn Gln Leu Asn Tyr Gly Glu Tyr Leu Tyr Glu Leu  
 245 250 255  
 Gly Leu Ile Asp Leu Asn Gly Arg Lys Lys Phe Asp Glu Asp Thr Ala  
 260 265 270  
 Ala Ala Ile Ala Cys Ala Glu Arg Lys Asp Met Asn Ser Ala Asn Arg  
 275 280 285  
 Leu Ile Gln Gly Leu Phe Asp Gly Leu Asp Gly Gln Glu Ser Tyr Phe  
 290 295 300  
 Lys Lys Val Thr Gly Phe Ser Ser Tyr Tyr Asn Phe Ile Lys Gly Asp  
 305 310 315 320  
 Glu Glu Ser Lys Gln Asp Ser Val Leu Met Glu Phe Leu Ser Asn Pro  
 325 330 335  
 Glu Val Arg Lys Gly Ile His Val Gly Glu Leu Pro Phe His Asp Ser  
 340 345 350  
 Asp Gly His Asn Lys Val Ala Glu Met Leu Ser Glu Asp Thr Leu Asp  
 355 360 365  
 Thr Val Ala Pro Trp Val Ser Lys Leu Leu Ser His Tyr Arg Val Leu  
 370 375 380  
 Phe Tyr Asn Gly Gln Leu Asp Ile Ile Cys Ala Tyr Pro Met Thr Val  
 385 390 395 400  
 Asp Phe Leu Met Lys Met Pro Phe Asp Gly Asp Ser Glu Tyr Lys Arg  
 405 410 415  
 Ala Asn Arg Glu Ile Tyr Arg Val Asp Gly Glu Ile Ala Gly Tyr Lys  
 420 425 430  
 Lys Arg Ala Gly Arg Leu Gln Glu Val Leu Ile Arg Asn Ala Gly His  
 435 440 445  
 Met Val Pro Arg Asp Gln Pro Lys Trp Ala Phe Asp Met Ile Thr Ser  
 450 455 460  
 Phe Thr His Lys Asn Tyr Leu  
 465 470

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 190283

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ile Arg Ala Ala Pro Pro Pro Leu Phe Leu Leu Leu Leu Leu  
 1 5 10 15  
 Leu Leu Leu Val Ser Trp Ala Ser Arg Gly Glu Ala Ala Pro Asp Gln  
 20 25 30  
 Asp Glu Ile Gln Arg Leu Pro Gly Leu Ala Lys Gln Pro Ser Phe Arg  
 35 40 45



Gln Tyr Ser Gly Tyr Leu Lys Ser Ser Gly Ser Lys His Leu His Tyr																	
50						55					60						
Trp Phe Val Glu Ser Gln Lys Asp Pro Glu Asn Ser Pro Val Val Leu						70					75						80
65																	
Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Asp Gly Leu Leu Thr						85					90						95
35																	
Glu His Gly Pro Phe Leu Val Gln Pro Asp Gly Val Thr Leu Glu Tyr						100					105						110
100																	
Asn Pro Tyr Ser Trp Asn Leu Ile Ala Asn Val Leu Tyr Leu Glu Ser						115					120						125
115																	
Pro Ala Gly Val Gly Phe Ser Tyr Ser Asp Asp Lys Phe Tyr Ala Thr						120					125						
120																	
Asn Asp Thr Glu Val Ala Gln Ser Asn Phe Glu Ala Leu Gln Asp Phe						135					140						
135																	
Phe Arg Leu Phe Pro Glu Tyr Lys Asn Asn Lys Leu Phe Leu Thr Gly						145					150						155
145																	
Glu Ser Tyr Ala Gly Ile Tyr Ile Pro Thr Leu Ala Val Leu Val Met						155					160						
155																	
Gln Asp Pro Ser Met Asn Leu Gln Gly Leu Ala Val Gly Asn Gly Leu						165					170						
165																	
Ser Ser Tyr Glu Gln Asn Asp Asn Ser Leu Val Tyr Phe Ala Tyr Tyr						175					180						
175																	
His Gly Leu Leu Gly Asn Arg Leu Trp Ser Ser Leu Gln Thr His Cys						185					190						
185																	
Cys Ser Gln Asn Lys Cys Asn Phe Tyr Asp Asn Lys Asp Leu Glu Cys						195					200						
195																	
Val Thr Asn Leu Gln Glu Val Ala Arg Ile Val Gly Asn Ser Gly Leu						205					210						
205																	
Asn Ile Tyr Asn Leu Tyr Ala Pro Cys Ala Gly Gly Val Pro Ser His						215					220						
215																	
Phe Arg Tyr Glu Lys Asp Thr Val Val Val Gln Asp Leu Gly Asn Ile						225					230						
225																	
Phe Thr Arg Leu Pro Leu Lys Arg Met Trp His Gln Ala Leu Leu Arg						235					240						
235																	
Ser Gly Asp Lys Val Arg Met Asp Pro Pro Cys Thr Asn Thr Thr Ala						245					250						
245																	
Ala Ser Thr Tyr Leu Asn Asn Pro Tyr Val Arg Lys Ala Leu Asn Ile						255					260						
255																	
Pro Glu Gln Leu Pro Gln Trp Asp Met Cys Asn Phe Leu Val Asn Leu						265					270						
265																	
Gln Tyr Arg Arg Leu Tyr Arg Ser Met Asn Ser Gln Tyr Leu Lys Leu						275					280						
275																	
Leu Ser Ser Gln Lys Tyr Gln Ile Leu Leu Tyr Asn Gly Asp Val Asp						285					290						
285																	
Met Ala Cys Asn Phe Met Gly Asp Glu Trp Phe Val Asp Ser Leu Asn						295					300						
295																	
Gln Lys Met Glu Val Gln Arg Arg Pro Trp Leu Val Lys Tyr Gly Asp						305					310						
305																	
Ser Gly Asp Lys Val Arg Met Asp Pro Pro Cys Thr Asn Thr Thr Ala						315					320						
315																	
Ala Ser Thr Tyr Leu Asn Asn Pro Tyr Val Arg Lys Ala Leu Asn Ile						325					330						
325																	
Pro Glu Gln Leu Pro Gln Trp Asp Met Cys Asn Phe Leu Val Asn Leu						335					340						
335																	
Gln Tyr Arg Arg Leu Tyr Arg Ser Met Asn Ser Gln Tyr Leu Lys Leu						345					350						
345																	
Leu Ser Ser Gln Lys Tyr Gln Ile Leu Leu Tyr Asn Gly Asp Val Asp						355					360						
355																	
Met Ala Cys Asn Phe Met Gly Asp Glu Trp Phe Val Asp Ser Leu Asn						365					370						
365																	
Gln Lys Met Glu Val Gln Arg Arg Pro Trp Leu Val Lys Tyr Gly Asp						375					380						
375																	
Ser Gly Glu Gln Ile Ala Gly Phe Val Lys Glu Phe Ser His Ile Ala						385					390						
385																	
Phe Leu Thr Ile Lys Gly Ala Gly His Met Val Pro Thr Asp Lys Pro						395					400						
395																	
Leu Ala Ala Phe Thr Met Phe Ser Arg Phe Leu Asn Lys Gln Pro Tyr						405					410						
405																	